

#5

CB



PCT10

#9

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/088,960

DATE: 01/30/2003

TIME: 12:19:07

Input Set : A:\EP.txt

Output Set: N:\CRF4\01302003\J088960.raw

3 <110> APPLICANT: Luo, Ying
4 Mancebo, Halena
6 <120> TITLE OF INVENTION: NOVEL SYK KINASE-ASSOCIATED CELL CYCLE PROTEINS,
COMPOSITIONS, AND
7 METHODS OF USE
9 <130> FILE REFERENCE: A-68412-1/RMS/DHR
11 <140> CURRENT APPLICATION NUMBER: US 10/088,960
12 <141> CURRENT FILING DATE: 2002-03-22
14 <150> PRIOR APPLICATION NUMBER: US 09/404,967
15 <151> PRIOR FILING DATE: 1999-09-24
17 <150> PRIOR APPLICATION NUMBER: PCT/US 00/26338
18 <151> PRIOR FILING DATE: 2000-09-25
20 <160> NUMBER OF SEQ ID NOS: 12
22 <170> SOFTWARE: PatentIn version 3.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 3955
26 <212> TYPE: DNA
27 <213> ORGANISM: Homo sapiens
29 <220> FEATURE:
30 <221> NAME/KEY: misc_feature
31 <222> LOCATION: (1473)..(1473)
32 <223> OTHER INFORMATION: "n" at position 1473 can be any base.
35 <400> SEQUENCE: 1

P.6

ENTERED

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38	cccggcg	tcc	gccgc	ct	catggccc	gg	gccgccc	gac	acgagc	gg	cg	ctgagg	120
40	ccgcgtg	gag	ac	gtgagg	cg	gccgccc	gtg	ccctcac	agt	cggcg	tttc	cg	180
42	gcggtg	cccc	cg	cacgc	ctg	ccgccat	cg	cttcgc	g	g	g	g	240
44	tcccagg	ccc	gc	gcgc	gc	tccttg	gag	tcggc	g	g	g	g	300
46	agggcgc	gag	ag	ccgggc	gc	caccgc	gc	gccgc	gc	ccgc	gc	g	360
48	gtggagc	aga	ctg	ctg	ca	gcagag	cg	gcgcaga	agc	accag	ca	g	420
50	caactga	gag	aa	attac	gg	gattaat	gac	acccaga	tac	agca	agc	cttga	480
52	agtaatg	gaa	actt	gga	att	agcagt	gg	ctt	ctt	actg	cga	aga	540
54	cagcagg	agg	ag	aca	actt	ctac	caa	aca	gcactt	ctt	gca	atg	600
56	gtggga	agcc	aag	ca	gatac	aa	atgt	gatt	gatct	ca	ctg	gag	660
58	cagaga	a	caa	ttg	cttg	ttt	ggcc	gaa	tcaa	ac	agg	g	720
60	actgat	gag	a	ca	agcc	at	tag	ca	gatt	ctt	ga	ag	780
62	tgtttg	a	aga	gg	ac	ctac	aga	ag	ttt	g	agg	g	840
64	agacagg	aca	aag	ctccc	gt	tggg	ctaa	ag	aatgt	tgg	ca	at	900
66	gttattc	agt	catt	attt	aa	tctttt	gg	aa	tttag	a	ag	at	960
68	ccatcaa	atg	ctca	agatt	t	acccc	gaa	ac	caaa	agga	ac	at	1020
70	cgtgag	ctga	ggtat	ctatt	tgc	actt	ctt	gttg	gt	tacca	aa	ag	1080
72	tcaagag	cag	ttg	aaatt	ct	taag	gat	gct	ttcaa	at	ca	gc	1140
74	gtgagt	gag	ttac	acac	aa	attatt	ag	tggt	taga	ag	atgc	tt	1200
76	gaagagg	aga	cggat	ga	ga	agcc	aa	ag	aacccc	at	g	ct	1260

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W--> 78 ttccctggctg tgggagtact tgaaggtaaa aaatttgaaa acactgaaat gtttggtcag 1320
80 taccacttc aggtcaatgg gttcaaagat ctgcatgagt gcctagaagc tgcaatgatt 1380
82 gaaggagaaa ttgagtcttt acattcagag aattcaggaa aatcaggcca agagcattgg 1440
84 ttactggat taccacctgt gttaacattt ganttgtaa gatttgaatt taatcaggca 1500
86 ttgggaagac cagaaaaaat tcacaacaaa ttagaatttc cccaagtttt atatttggac 1560
88 agatacatgc acagaaacag agaaataaca agaattaaga gggaagagat caagagactg 1620
90 aaagattacc tcacggtatt acaacaaagg ctagaaagat atttaagcta tgggtccggt 1680
92 cccaaacgat tccccttggg agatgttctt cagtatgcat tgggaatttg ctcaagtaaa 1740
94 cctgtttgca cttctcctgt tgacgatatt gacgctagtt cccacacctag tggttccata 1800
96 ccatcacaga cattaccaag cacaacagaa caacaggggag ccctatcttc agaactgcc 1860
98 agcacatcac cttcatcagt tgctgccatt tcatcgagat cagtaataca caaaccattt 1920
100 actcagtcctc ggatacctcc agatttgccc atgcatccgg caccaaggca cataacggag 1980
102 gaagaacttt ctgtgctgga aagttgttta catcgctgga ggacagaaat agaaaatgac 2040
104 accagagatt tgcaggaaaag catatccaga atccatcgaa caattgaatt aatgtactct 2100
106 gacaaatcta tgatacaagt tccttatcga ttacatgccg ttttagttca cgaaggccaa 2160
108 gctaattgctg ggcactactg ggcataatatt tttgatcatc gtgaaagcag atggatgaag 2220
110 tacaatgata ttgctgtgac aaaatcatca tgggaagagc tagtgaggga ctcttttggg 2280
112 ggttatagaa atgccagtg atactgttta atgtacataa atgataaggc acagttccta 2340
114 atacaagagg agtttaataa agaaactggg cagccccttg ttggtataga aacattacca 2400
116 ccggtattga gagattttgt tgaggaagac aaccaacgat ttgaaaaaga actagaagaa 2460
118 tgggatgcac aacttgccca gaaagctttg caggaaaagc ttttagcgtc tcagaaattg 2520
120 agagatgcag agacttctgt gacaacagca caagcagcag gagaccaga atatctagag 2580
122 cagccatcaa gaagtgttt ctcaaagcac ttgaaagaag aaactattca aataattacc 2640
124 aaggcatcac atgagcatga agataaaagt cctgaaacag ttttgcagtc ggcaattaag 2700
126 ttggaatatg caaggttggg taagttggcc caagaagaca ccccaccaga aaccgattat 2760
128 cgtttacatc atgtagtggg ctactttatc cagaaccagg caccaaagaa aattattgag 2820
130 aaaacattac tagaacaatt tggagataga aatttgagtt ttgatgaaag gtgtcacaa 2880
132 ataataaag ttgctcaagc caaactggaa atgataaaac ctgaagaagt aaacttggag 2940
134 gaatatgagg agtggcatca ggattatagg aaattcaggg aaacaactat gtatctcata 3000
136 attgggctag aaaattttca aagagaaagt tatatagatt ccttgctgtt cctcatctgt 3060
138 gcttatcaga ataacaaaga actcttgtct aaaggcttat acagaggaca tgatgaagaa 3120
140 ttgatatcac attatagaag agaagtgttg ctaaaattaa atgagcaagc cgcagaactc 3180
142 ttggaatctg gagaggatcg agaagtaaac aatgggttga ttatcatgaa tgagtttatt 3240
144 gtcccatttt tgccattatt actggtggat gaaatggaag aaaaggatat actagctgta 3300
146 gaagatatga gaaatcgatg gtgttcctac cttggtcaag aaatggaacc acacctccaa 3360
148 gaaaagctga cagatttttt gccaaaactg cttgattgtt ctatggagat taaaagtttc 3420
150 catgagccac cgaagtacc ttcataattcc acgcatgaac tctgtgagcg atttgcccga 3480
152 atcatgttgt ccctcagtcg aactcctgct gatggaagat aaactgcaca ctttccttga 3540
154 acacactgta taaactcttt ttagttctta acccttgctt tctgtcaca gggtttgctt 3600
156 gttgctgcta tagtttttaa ctttttttta ttttaataac tgcaaaagac aaaatgacta 3660
158 tacagacttt agtcagactg cagacaataa agctgaaaat cgcagggcgc tcagacattt 3720
160 taaccggaac tgatgtataa tcacaaatct aattgatttt attatggcaa aactatgctt 3780
162 ttgccacctt cctgttgagc tattactttg cttttatctt ttctttctca acagctttcc 3840
164 attcagctcg gatccttcca tgactacagc catttaagtg ttcagcactg tgtacgatac 3900
166 ataataattg gtagcttgta aatgaaataa agaataaagt tttatttatg gctac 3955
169 <210> SEQ ID NO: 2
170 <211> LENGTH: 1055
171 <212> TYPE: PRT
172 <213> ORGANISM: Homo sapiens

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Input Set : A:\EP.txt

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174 <220> FEATURE:

175 <221> NAME/KEY: MISC_FEATURE

176 <222> LOCATION: (373)..(373)

177 <223> OTHER INFORMATION: "Xaa" at position 373 can be any amino acid.

180 <400> SEQUENCE: 2

182 Met Thr Val Glu Gln Asn Val Leu Gln Gln Ser Ala Ala Gln Lys His

183 1 5 10 15

186 Gln Gln Thr Phe Leu Asn Gln Leu Arg Glu Ile Thr Gly Ile Asn Asp

187 20 25 30

190 Thr Gln Ile Leu Gln Gln Ala Leu Lys Asp Ser Asn Gly Asn Leu Glu

191 35 40 45

194 Leu Ala Val Ala Phe Leu Thr Ala Lys Asn Ala Lys Thr Pro Gln Gln

195 50 55 60

198 Glu Glu Thr Thr Tyr Tyr Gln Thr Ala Leu Pro Gly Asn Asp Arg Tyr

199 65 70 75 80

202 Ile Ser Val Gly Ser Gln Ala Asp Thr Asn Val Ile Asp Leu Thr Gly

203 85 90 95

206 Asp Asp Lys Asp Asp Leu Gln Arg Thr Ile Ala Leu Ser Leu Ala Glu

207 100 105 110

210 Ser Asn Arg Ala Phe Arg Glu Thr Gly Ile Thr Asp Glu Glu Gln Ala

211 115 120 125

214 Ile Ser Arg Val Leu Glu Ala Ser Ile Ala Glu Asn Lys Ala Cys Leu

215 130 135 140

218 Lys Arg Thr Pro Thr Glu Val Trp Arg Asp Ser Arg Asn Pro Tyr Asp

219 145 150 155 160

222 Arg Lys Arg Gln Asp Lys Ala Pro Val Gly Leu Lys Asn Val Gly Asn

223 165 170 175

226 Thr Cys Trp Phe Ser Ala Val Ile Gln Ser Leu Phe Asn Leu Leu Glu

227 180 185 190

230 Phe Arg Arg Leu Val Leu Asn Tyr Lys Pro Pro Ser Asn Ala Gln Asp

231 195 200 205

234 Leu Pro Arg Asn Gln Lys Glu His Arg Asn Leu Pro Phe Met Arg Glu

235 210 215 220

238 Leu Arg Tyr Leu Phe Ala Leu Leu Val Gly Thr Lys Arg Lys Tyr Val

239 225 230 235 240

242 Asp Pro Ser Arg Ala Val Glu Ile Leu Lys Asp Ala Phe Lys Ser Asn

243 245 250 255

246 Asp Ser Gln Gln Gln Asp Val Ser Glu Phe Thr His Lys Leu Leu Asp

247 260 265 270

250 Trp Leu Glu Asp Ala Phe Gln Met Lys Ala Glu Glu Glu Thr Asp Glu

251 275 280 285

254 Glu Lys Pro Lys Asn Pro Met Val Glu Leu Phe Tyr Gly Arg Phe Leu

255 290 295 300

258 Ala Val Gly Val Leu Glu Gly Lys Lys Phe Glu Asn Thr Glu Met Phe

259 305 310 315 320

262 Gly Gln Tyr Pro Leu Gln Val Asn Gly Phe Lys Asp Leu His Glu Cys

263 325 330 335

266 Leu Glu Ala Ala Met Ile Glu Gly Glu Ile Glu Ser Leu His Ser Glu

267 340 345 350

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Input Set : A:\EP.txt

Output Set: N:\CRF4\01302003\J088960.raw

```

270 Asn Ser Gly Lys Ser Gly Gln Glu His Trp Phe Thr Gly Leu Pro Pro
271      355      360      365
W--> 274 Val Leu Thr Phe Xaa Leu Ser Arg Phe Glu Phe Asn Gln Ala Leu Gly
275      370      375      380
278 Arg Pro Glu Lys Ile His Asn Lys Leu Glu Phe Pro Gln Val Leu Tyr
279 385      390      395      400
282 Leu Asp Arg Tyr Met His Arg Asn Arg Glu Ile Thr Arg Ile Lys Arg
283      405      410      415
286 Glu Glu Ile Lys Arg Leu Lys Asp Tyr Leu Thr Val Leu Gln Gln Arg
287      420      425      430
290 Leu Glu Arg Tyr Leu Ser Tyr Gly Ser Gly Pro Lys Arg Phe Pro Leu
291      435      440      445
294 Val Asp Val Leu Gln Tyr Ala Leu Glu Phe Ala Ser Ser Lys Pro Val
295      450      455      460
298 Cys Thr Ser Pro Val Asp Asp Ile Asp Ala Ser Ser Pro Pro Ser Gly
299 465      470      475      480
302 Ser Ile Pro Ser Gln Thr Leu Pro Ser Thr Thr Glu Gln Gln Gly Ala
303      485      490      495
306 Leu Ser Ser Glu Leu Pro Ser Thr Ser Pro Ser Ser Val Ala Ala Ile
307      500      505      510
310 Ser Ser Arg Ser Val Ile His Lys Pro Phe Thr Gln Ser Arg Ile Pro
311      515      520      525
314 Pro Asp Leu Pro Met His Pro Ala Pro Arg His Ile Thr Glu Glu Glu
315      530      535      540
318 Leu Ser Val Leu Glu Ser Cys Leu His Arg Trp Arg Thr Glu Ile Glu
319 545      550      555      560
322 Asn Asp Thr Arg Asp Leu Gln Glu Ser Ile Ser Arg Ile His Arg Thr
323      565      570      575
326 Ile Glu Leu Met Tyr Ser Asp Lys Ser Met Ile Gln Val Pro Tyr Arg
327      580      585      590
330 Leu His Ala Val Leu Val His Glu Gly Gln Ala Asn Ala Gly His Tyr
331      595      600      605
334 Trp Ala Tyr Ile Phe Asp His Arg Glu Ser Arg Trp Met Lys Tyr Asn
335      610      615      620
338 Asp Ile Ala Val Thr Lys Ser Ser Trp Glu Glu Leu Val Arg Asp Ser
339 625      630      635      640
342 Phe Gly Gly Tyr Arg Asn Ala Ser Ala Tyr Cys Leu Met Tyr Ile Asn
343      645      650      655
346 Asp Lys Ala Gln Phe Leu Ile Gln Glu Glu Phe Asn Lys Glu Thr Gly
347      660      665      670
350 Gln Pro Leu Val Gly Ile Glu Thr Leu Pro Pro Asp Leu Arg Asp Phe
351      675      680      685
354 Val Glu Glu Asp Asn Gln Arg Phe Glu Lys Glu Leu Glu Glu Trp Asp
355      690      695      700
358 Ala Gln Leu Ala Gln Lys Ala Leu Gln Glu Lys Leu Leu Ala Ser Gln
359 705      710      715      720
362 Lys Leu Arg Glu Ser Glu Thr Ser Val Thr Thr Ala Gln Ala Ala Gly
363      725      730      735
366 Asp Pro Glu Tyr Leu Glu Gln Pro Ser Arg Ser Asp Phe Ser Lys His

```

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DATE: 01/30/2003

TIME: 12:19:07

Input Set : A:\EP.txt

Output Set: N:\CRF4\01302003\J088960.raw

```

367          740          745          750
370 Leu Lys Glu Thr Ile Gln Ile Ile Thr Lys Ala Ser His Glu His
371          755          760          765
374 Glu Asp Lys Ser Pro Glu Thr Val Leu Gln Ser Ala Ile Lys Leu Glu
375          770          775          780
378 Tyr Ala Arg Leu Val Lys Leu Ala Gln Glu Asp Thr Pro Pro Glu Thr
379 785          790          795          800
382 Asp Tyr Arg Leu His His Val Val Val Tyr Phe Ile Gln Asn Gln Ala
383          805          810          815
386 Pro Lys Lys Ile Ile Glu Lys Thr Leu Leu Glu Gln Phe Gly Asp Arg
387          820          825          830
390 Asn Leu Ser Phe Asp Glu Arg Cys His Asn Ile Met Lys Val Ala Gln
391          835          840          845
394 Ala Lys Leu Glu Met Ile Lys Pro Glu Glu Val Asn Leu Glu Glu Tyr
395          850          855          860
398 Glu Glu Trp His Gln Asp Tyr Arg Lys Phe Arg Glu Thr Thr Met Tyr
399 865          870          875          880
402 Leu Ile Ile Gly Leu Glu Asn Phe Gln Arg Glu Ser Tyr Ile Asp Ser
403          885          890          895
406 Leu Leu Phe Leu Ile Cys Ala Tyr Gln Asn Asn Lys Glu Leu Leu Ser
407          900          905          910
410 Lys Gly Leu Tyr Arg Gly His Asp Glu Glu Leu Ile Ser His Tyr Arg
411          915          920          925
414 Arg Glu Cys Leu Leu Lys Leu Asn Glu Gln Ala Ala Glu Leu Phe Glu
415          930          935          940
418 Ser Gly Glu Asp Arg Glu Val Asn Asn Gly Leu Ile Ile Met Asn Glu
419 945          950          955          960
422 Phe Ile Val Pro Phe Leu Pro Leu Leu Leu Val Asp Glu Met Glu Glu
423          965          970          975
426 Lys Asp Ile Leu Ala Val Glu Asp Met Arg Asn Arg Trp Cys Ser Tyr
427          980          985          990
430 Leu Gly Gln Glu Met Glu Pro His Leu Gln Glu Lys Leu Thr Asp Phe
431          995          1000          1005
434 Leu Pro Lys Leu Leu Asp Cys Ser Met Glu Ile Lys Ser Phe His
435          1010          1015          1020
438 Glu Pro Pro Lys Leu Pro Ser Tyr Ser Thr His Glu Leu Cys Glu
439          1025          1030          1035
442 Arg Phe Ala Arg Ile Met Leu Ser Leu Ser Arg Thr Pro Ala Asp
443          1040          1045          1050
446 Gly Arg
447          1055
450 <210> SEQ ID NO: 3
451 <211> LENGTH: 4015
452 <212> TYPE: DNA
453 <213> ORGANISM: Homo sapiens
455 <220> FEATURE:
456 <221> NAME/KEY: misc_feature
457 <222> LOCATION: (1473)..(1473)
458 <223> OTHER INFORMATION: "n" at position 1473 can be any base.

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/088,960

DATE: 01/30/2003
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Input Set : A:\EP.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 1473
Seq#:2; Xaa Pos. 373
Seq#:3; N Pos. 1473
Seq#:4; Xaa Pos. 373
Seq#:5; Xaa Pos. 373

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:6,7